UNIVERSITI TEKNOLOGI MARA

ANALYSIS OF Y-CHROMOSOMAL SHORT TANDEM REPEAT (Y-STR) POLYMORPHISMS AMONG ORANG ASLI POPULATION IN TAMAN NEGARA AND JERANTUT OF PAHANG

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of the requirementsfor the degree of
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AUTHOR'S DECLARATION

I declare that the work in this thesis was carried out in accordance with the regulations of Universiti Teknologi MARA. It is original and is the result of my own work, unless otherwise indicated or acknowledged as referenced work. This thesis has not been submitted to any other academic institution or non-academic institution for any other degree or qualification.

I, hereby, acknowledge that I have been supplied with the Academic Rules and Regulations for Post Graduate, Universiti Teknologi MARA, regulating the conduct of my study and research.

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ABSTRACT

Orang Asli in Peninsular Malaysia have different types of culture and belief, which impacted from history of migration centuries ago. They are three major sub-ethnic groups namely Negrito, Senoi and Proto-Malay. The main goal of this research is to study the genetic variation among Orang Asli population in Taman Negara and Jerantut area by investigating their polymorphisms on Y-chromosome. Male genomic DNA samples of 228 Orang Asli descendants (Batek, Semaq Beri and Jah Hut tribes) from Taman Negara and Jerantut rural area of Pahang were extracted from the buccal swab samples. Four different Y-STR loci namely DYS 19, DYS 390, DYS 391 and DYS 392 were tested. All samples were amplified through Polymerase Chain Reaction and the products were separated by 1.5% agarose gel electrophoresis. The individual allele frequencies and four Y-STR haplotype frequencies for each locus were determined. Apart from that, gene diversity (GD), locus diversity (D_L), haplotype diversity (HD) and discrimination capacity (DC) were calculated among the three tribes. Allele frequency among the three tribes appeared to be imbalanced. The significant differences of gene diversity (GD) were observed in DYS 390 locus (0.7593) across the tribes, whilst Batek (0.7076) across the loci. After matching criteria of length and homogeneity, all of the loci tested proved to be polymorphic and the diversity of individual loci (D_L) ranges from 0.6597 to 0.7877. Results revealed a number of 111 different haplotypes, of which 68 were unique and appeared only once. The overall haplotypes diversity (HD) for four Y-STR loci in this study was 0.9946 with discrimination capacity (DC) of 0.4868. F-statistics analysis indicated that 57.3% of the haplotypic variation was found within tribes and 42.7% was distributed between tribes. However, errors of scoring and factors like small sample size and limited Y-STR markers tested should be considered. This research can contribute valuable information in future, where the variation of Y-chromosome in this study with combination of other tribe's data can be used to construct phylogenetic tree of Orang Asli in Malaysia.

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